What is claimed is:

1. An isolated nucleic acid molecule comprising SEQ ID NO: 1, an oligonucleotide of about 10 to about 50 nucleotides of SEQ ID NO: 1, SEQ ID NO: 3, an oligonucleotide of about 10 to about 50 nucleotides of SEQ ID NO: 3, SEQ ID NO: 5, an oligonucleotide of about 10 to about 50 nucleotides of SEQ ID NO: 5, or a complement of one of the foregoing nucleic acid molecules, wherein the nucleic acid molecule has an alteration in at least one nucleotide, and wherein the alteration is indicative of the presence of an optineurin-associated glaucoma or of an optineurin-associated risk of glaucoma.

2. The isolated nucleic acid molecule of Claim 1, wherein the alteration produces a sequence change in a polypeptide encoded by the nucleic acid molecule.

3. The isolated nucleic acid molecule of Claim 2, wherein the alteration is a change from GAG to AAG at codon 50, an insertion of AG after codon 127, a change from CGG to CAG at codon 545, a change from ATG to AAG at codon 98, a change from CCC to GCC at codon 16, a change from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, a change from GAA to AAA at codon 322, a complement of one of the foregoing alterations, or a combination comprising one or more of the foregoing alterations.

4. The isolated nucleic acid of Claim 1, wherein the glaucoma is primary open angle glaucoma.

5. A purified polypeptide comprising SEQ ID NO: 2, a peptide of about 10 to about 50 contiguous amino acids of SEQ ID NO: 2, SEQ ID NO: 4, a peptide of about 10 to about 50 contiguous amino acids of SEQ ID NO: 4, SEQ ID NO: 6, or a peptide of about 10 to about 50 contiguous amino acids of SEQ ID NO: 6, wherein the polypeptide has an alteration in at least one amino acid, and wherein the alteration is indicative of the presence of an optineurin-associated glaucoma or of an optineurin-associated risk of glaucoma.

6. The purified polypeptide of Claim 5, wherein the alteration is a change from glutamic acid to lysine at codon 50, a premature stop after codon 127, a change from arginine to glutamine at codon 545, a change from methionine to lysine at codon 98, a change from proline to alanine at codon 16, a change from glutamine to histidine at codon 42, a change from glutamic acid to valine at codon 92, a change from glutamic acid to lysine at codon 322 or a combination comprising one or more of the foregoing alterations.

7. The purified polypeptide of Claim 5, wherein the glaucoma is primary open angle glaucoma.

8. An array of nucleic acid molecules attached to a solid support, the array comprising an oligonucleotide comprising about 10 to about 50 nucleotides of SEQ ID NO: 1, about 10 to about 50 nucleotides of SEQ ID NO: 3, about 10 to about 50 nucleotides of SEQ ID NO: 5, or a complement of one of the foregoing oligonucleotides, wherein the oligonucleotide has an alteration in at least one nucleotide, and wherein the alteration is indicative of the presence of an optineurin-associated glaucoma or of an optineurin-associated risk of glaucoma.

9. The array of Claim 8, wherein the alteration produces a sequence change in a polypeptide encoded by an optineurin nucleic acid molecule comprising the oligonucleotide.

10. The array of Claim 9, wherein the alteration is a change from GAG to AAG at codon 50, an insertion of AG after codon 127, a change from CGG to CAG at codon 545, a change from ATG to AAG at codon 98, a change from CCC to GCC at codon 16, a change from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, a change from GAA to AAA at codon 322, a complement of one of the foregoing alterations, or a combination comprising one or more of the foregoing alterations.

11. A method of detecting the presence or absence of an optineurin-associated glaucoma or an optineurin-associated risk of glaucoma in a sample from an individual, comprising assessing the sample for:

an alteration in an optineurin nucleic acid; or

an alteration in an optineurin polypeptide;

wherein the alteration in the optineurin nucleic acid or the alteration in the optineurin polypeptide is indicative of the presence or the absence of an optineurin-associated glaucoma or an optineurin-associated risk of glaucoma.

12. The method of Claim 11, wherein the alteration is in an optineurin nucleic acid.

13. The method of Claim 12, wherein the optineurin nucleic acid comprises at least a fragment of about 10 to about 50 nucleotides of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5.

14. The method of Claim 13, wherein the alteration is a change from GAG to AAG at codon 50, an insertion of AG after codon 127, a change from CGG to CAG at codon 545, a change from ATG to AAG at codon 98, a change from CCC to GCC at codon 16, a change from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, a change from GAA to AAA at codon 322, or a combination comprising one or more of the foregoing alterations.

15. The method of Claim 12, wherein assessing comprises sequencing at least a portion of a optineurin nucleic acid, or hybridizing a nucleic acid probe to a nucleic acid.

16. The method of Claim 12, wherein assessing comprises utilizing an array of nucleic acid molecules attached to a solid support.

17. The method of Claim 16, wherein at least one of the nucleic acid molecules is an oligonucleotide having an alteration in at least one nucleotide, and wherein the alteration is indicative of the presence of optineurin-associated glaucoma or of an optineurin-associated risk of glaucoma.

18. The method of Claim 11, wherein the alteration is in an optineurin polypeptide.

19. The method of Claim 18, wherein the alteration is a change from glutamic acid to lysine at codon 50, a premature stop after codon 127, a change from arginine to glutamine at codon 545, a change from methionine to lysine at codon 98, a change from proline to alanine at codon 16, a change from glutamine to histidine at codon 42, a change from glutamic acid to valine at codon 92, a change from glutamic acid to lysine at codon 322, or a combination comprising one or more of the foregoing alterations.

20. The method of Claim 11, comprising detecting an alteration in an optineurin nucleic acid or an optineurin polypeptide associated with the presence of optineurin-associated glaucoma.

21. The method of Claim 20, further comprising diagnosing optineurin-associated glaucoma in an individual.

22. The method of Claim 20, wherein the alteration is a change from GAG to AAG at codon 50, an insertion of AG after codon 127, a change from CGG to CAG at codon 545, or a combination comprising one or more of the foregoing alterations.

23. The method of Claim 11, comprising detecting an alteration in an optineurin nucleic acid or an optineurin polypeptide associated with the presence of an optineurin-associated risk of glaucoma.

24. The method of Claim 23, further comprising diagnosing an optineurin-associated risk of glaucoma in an individual.

25. The method of Claim 23, further comprising prognosing an optineurin-associated risk of glaucoma in an individual.

26. The method of Claim 23, wherein the alteration is a change from ATG to AAG at codon 98.

27. The method of Claim 11, comprising detecting the absence of an alteration in an optineurin nucleic acid and diagnosing the absence of an optineurin-associated glaucoma, an optineurin-associated risk of glaucoma, or both.

28. The method of Claim 11, wherein the glaucoma is a primary open angle glaucoma.

29. A method of diagnosing glaucoma or the risk of glaucoma in an individual comprising assessing a sample from the individual for an alteration in an optineurin nucleic acid, an alteration in an optineurin polypeptide, or both.

30. The method of Claim 29, wherein the optineurin nucleic acid comprises at least a fragment of about 10 to about 50 nucleotides of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5.

31. The method of Claim 30, wherein the alteration is a change from GAG to AAG at codon 50, an insertion of AG after codon 127, a change from CGG to CAG at codon 545, a change from ATG to AAG at codon 98, a change from CCC to GCC at codon 16, a change from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, a change from GAA to AAA at codon 322, or a combination comprising one or more of the foregoing alterations.

32. The method of Claim 29, wherein the optineurin polypeptide comprises at least an active fragment of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6.

33. The method of Claim 32, wherein the alteration is a change from glutamic acid to lysine at codon 50, a premature stop after codon 127, a change from arginine to glutamine at codon 545, a change from methionine to lysine at codon 98, a change from proline to alanine at codon 16, a change from glutamine to histidine at codon 42, a change from glutamic acid to valine at codon 92, a change from glutamic acid to lysine at codon 322, or a combination comprising one or more of the foregoing alterations.

34. A method of screening for glaucoma or the risk of glaucoma in an individual comprising assessing a sample from the individual for an alteration in an optineurin nucleic acid, an alteration in an optineurin polypeptide, or both.

35. The method of Claim 34, wherein the optineurin nucleic acid comprises at least a fragment of about 10 to about 50 nucleotides of SEQ ID NO: 1, SEQ ID NO: 3, or SEQ ID NO: 5.

36. The method of Claim 35, wherein the alteration is a change from GAG to AAG at codon 50, an insertion of AG after codon 127, a change from CGG to CAG at codon 545, a change from ATG to AAG at codon 98, a change from CCC to GCC at codon 16, a change from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, a change from GAA to AAA at codon 322, or a combination comprising one or more of the foregoing alterations.

37. The method of Claim 34, wherein the optineurin polypeptide comprises at least an active fragment of SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6.

38. The method of Claim 37, wherein the alteration is a change from glutamic acid to lysine at codon 50, a premature stop after codon 127, a change from arginine to glutamine at codon 545, a change from methionine to lysine at codon 98, a change from proline to alanine at codon 16, a change from glutamine to histidine at codon 42, a change from glutamic acid to valine at codon 92, a change from glutamic acid to lysine at codon 322, or a combination comprising one or more of the foregoing alterations.

39. A method of treating glaucoma in an individual, comprising administering to the individual an optineurin therapeutic agent in a therapeutically effective amount.

40. A method of treating an individual having an increased risk for glaucoma, comprising administering to the individual an optineurin therapeutic agent in a therapeutically or prophylacticly effective amount.

41. A computer readable medium comprising an optineurin nucleic acid sequence, an optineurin polypeptide sequence, or a combination thereof,

wherein the optineurin nucleic acid sequence comprises SEQ ID NO: 1, an oligonucleotide of about 10 to about 50 nucleotides of SEQ ID NO: 1, SEQ ID NO. 3, an oligonucleotide of about 10 to about 50 nucleotides of SEQ ID NO: 3, SEQ ID NO: 5, an oligonucleotide of about 10 to about 50 nucleotides of SEQ ID NO: 5, or the complement of one of the foregoing nucleic acid sequences, wherein the nucleic acid sequence has an alteration in at least one nucleotide, and wherein the alteration is indicative of the presence or absence of optineurin-associated glaucoma or of an optineurin-associated risk of glaucoma; and

wherein the optineurin polypeptide sequence comprises SEQ ID NO: 2, a peptide of about 10 to about 50 contiguous amino acids of SEQ ID NO: 2, SEQ ID NO. 4, a peptide of about 10 to about 50 contiguous amino acids of SEQ ID NO: 4, SEQ ID NO: 6, or a peptide of about 10 to about 50 contiguous amino acids of SEQ ID NO: 6, wherein the polypeptide sequence has an alteration in at least one amino acid, and wherein the alteration is indicative of the presence or absence of optineurin-associated glaucoma or of an optineurin-associated risk of glaucoma.

42. The computer readable medium of Claim 41, wherein the optineurin nucleic acid sequence comprises a change from GAG to AAG at codon 50, an insertion of AG after codon 127, a change from CGG to CAG at codon 545, a change from ATG to AAG at codon 98, a change from CCC to GCC at codon 16, a change from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, a change from GAA to AAA at codon 322, a complement of one of the foregoing alterations, or a combination comprising one or more of the foregoing alterations.

43. The computer readable medium of Claim 41, wherein the optineurin polypeptide sequence comprises a glutamic acid to lysine at codon 50, a premature stop after codon 127, an arginine to glutamine at codon 545, a methionine to lysine at codon 98, a proline to alanine at codon 16, a glutamine to histidine at codon 42, a glutamic acid to valine at codon 92, a glutamic acid to lysine at codon 322. or a combination comprising one or more of the foregoing alterations.